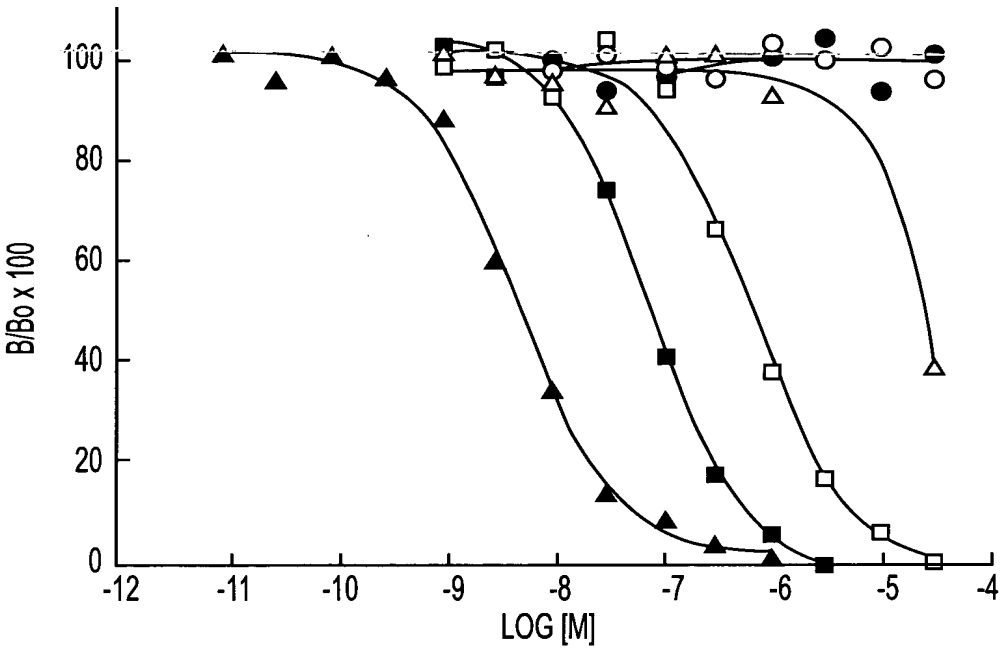


FIG. 1

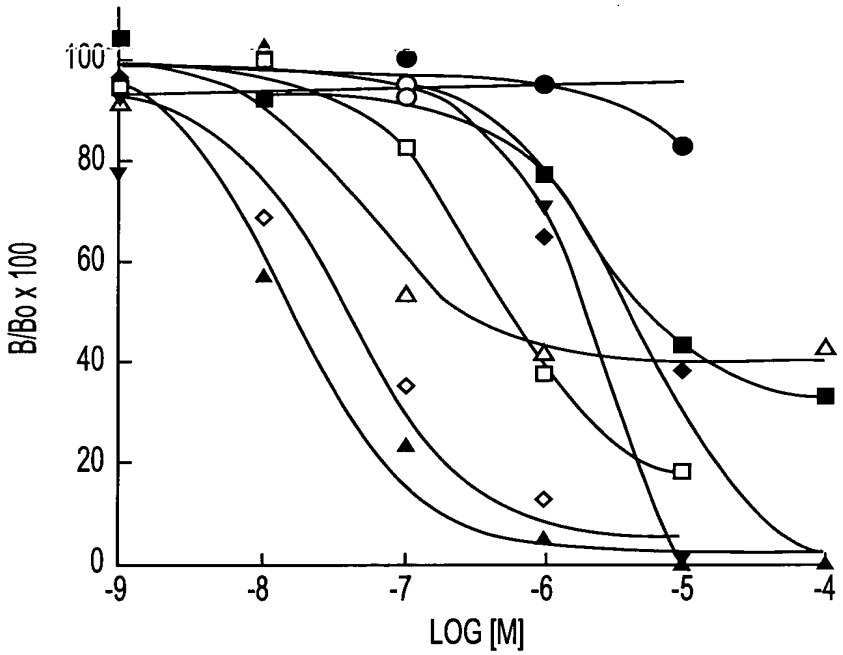


FIG. 2

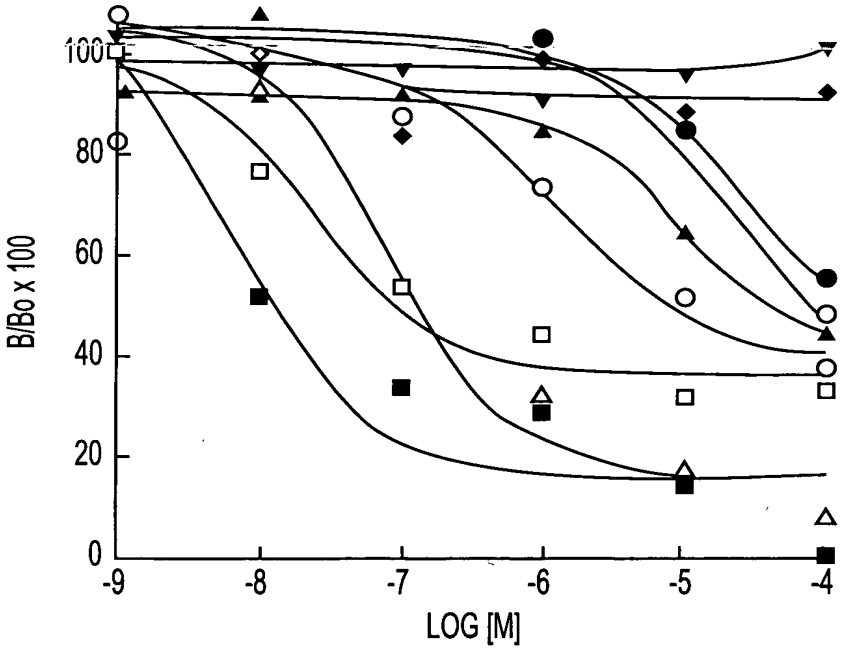


FIG. 3

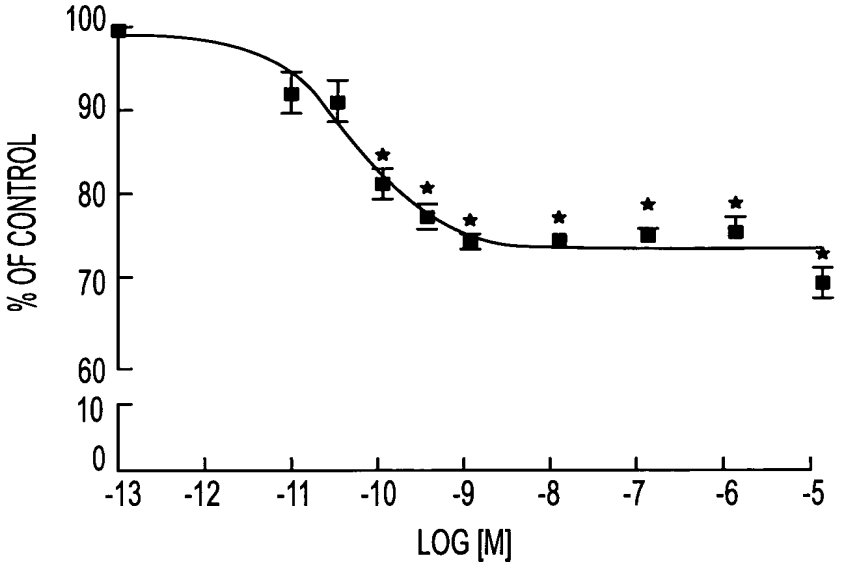


FIG. 4

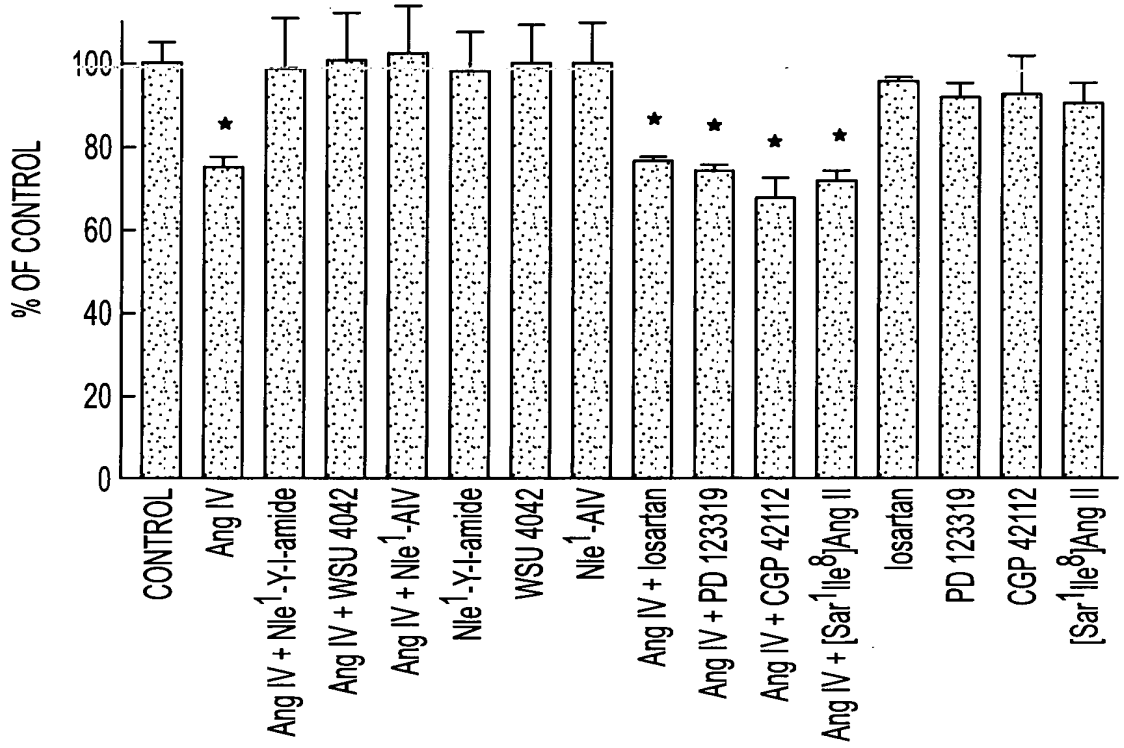
% OF CONTROL
100
80
60
40
20
0
CONTROL
Ang IV
Ang IV + Nle$^1$-Y-I-amide
Ang IV + WSU 4042
Ang IV + Nle$^1$-AIV
Nle$^1$-Y-I-amide
WSU 4042
Nle$^1$-AIV
Ang IV + losartan
Ang IV + PD 123319
Ang IV + CGP 42112
Ang IV + [Sar$^1$Ile$^8$]Ang II
losartan
PD 123319
CGP 42112
[Sar$^1$Ile$^8$]Ang II

FIG. 5

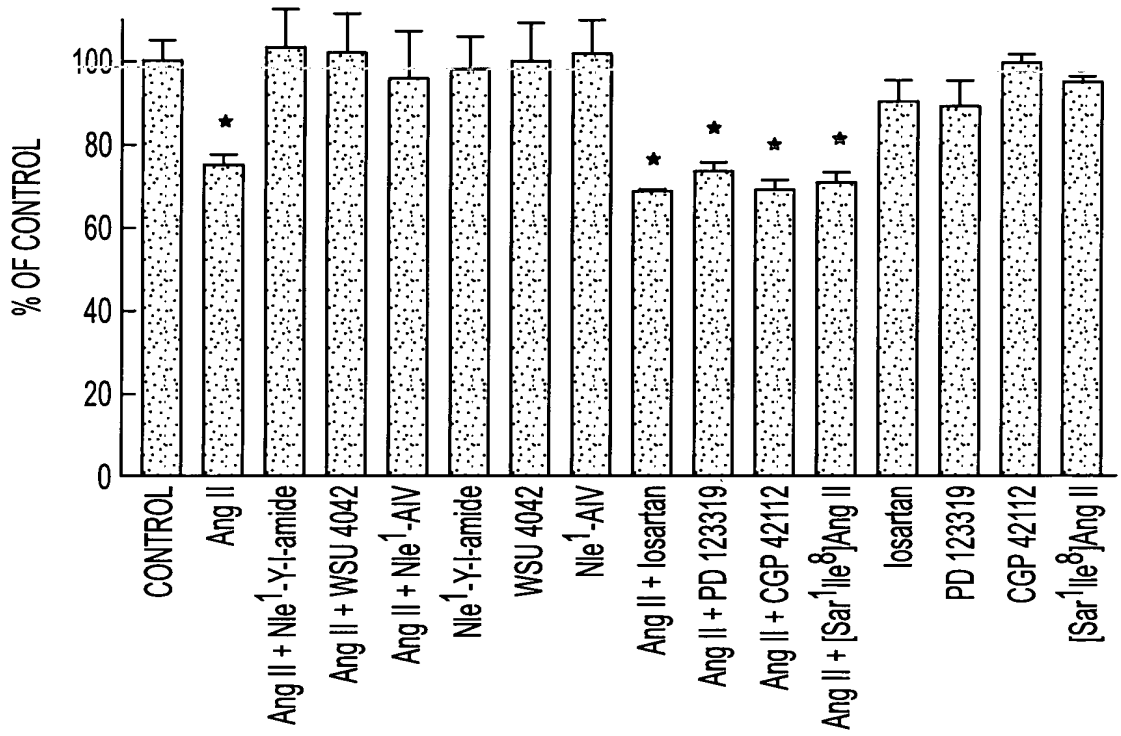
% OF CONTROL
100
80
60
40
20
0
CONTROL
Ang II
Ang II + Nle$^1$-Y-I-amide
Ang II + WSU 4042
Ang II + Nle$^1$-AIV
Nle$^1$-Y-I-amide
WSU 4042
Nle$^1$-AIV
Ang II + losartan
Ang II + PD 123319
Ang II + CGP 42112
Ang II + [Sar$^1$Ile$^8$]Ang II
losartan
PD 123319
CGP 42112
[Sar$^1$Ile$^8$]Ang II

FIG. 6

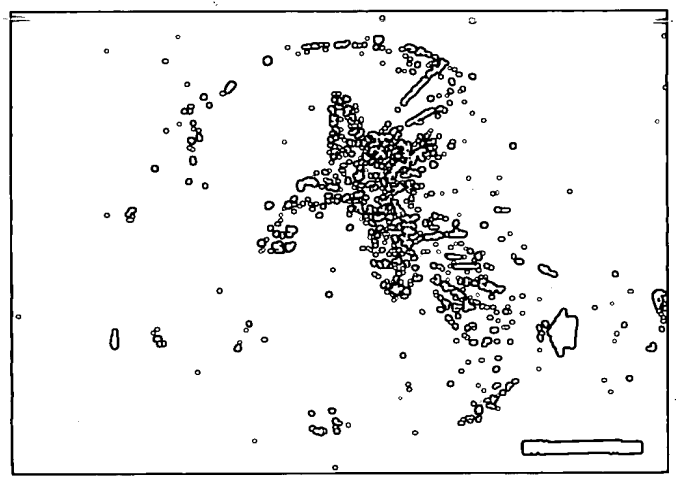

FIG. 7

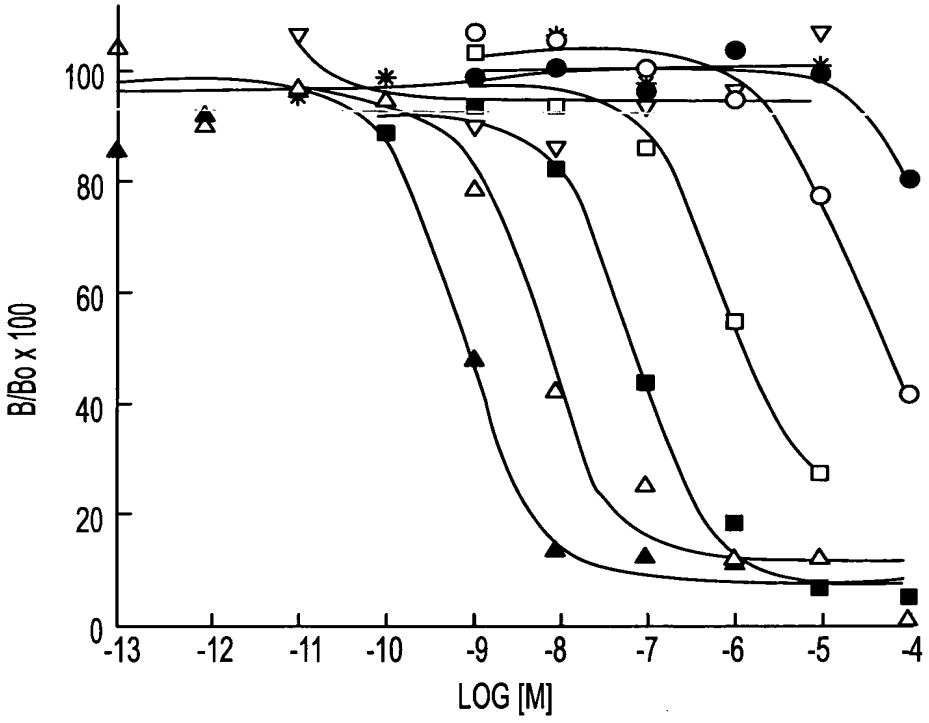


FIG. 8

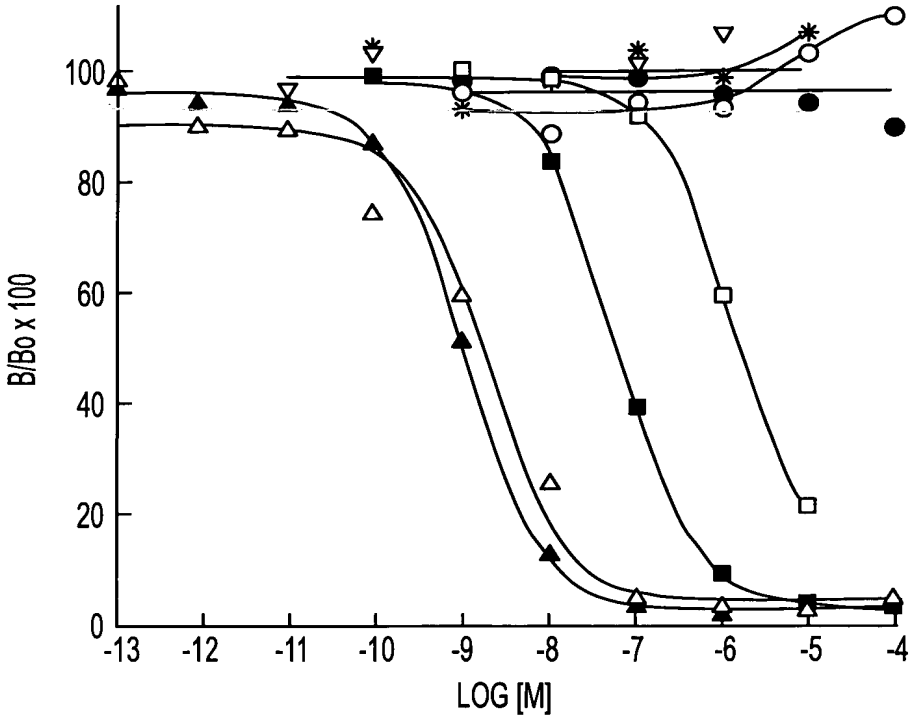


FIG. 9

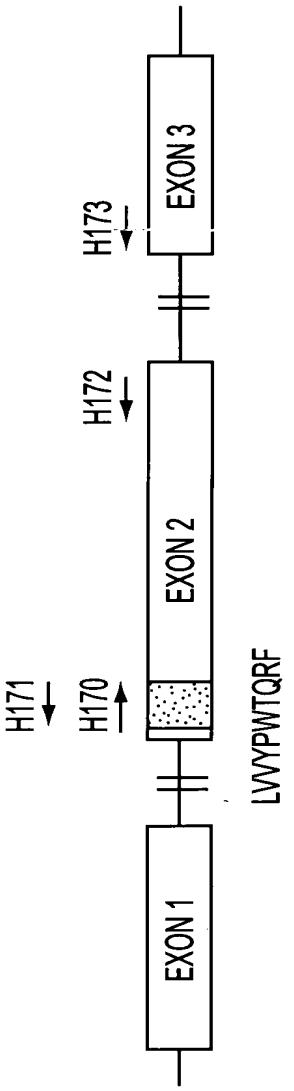


FIG. 10A

OLIGONUCLEOTIDE SEQUENCES:

H170: 5' CTGGTTGTCTACCCCTGGACTCAGAG 3'
H171: 5' CTCTGAGTCCAGGGGTAGACAACCAG 3'
H172: 5' CTCAGGATCCACATGCAGCTTATCACAG 3'
H173: 5' CAGCACAACCACTAGCACATTGCC 3'

FIG. 10B

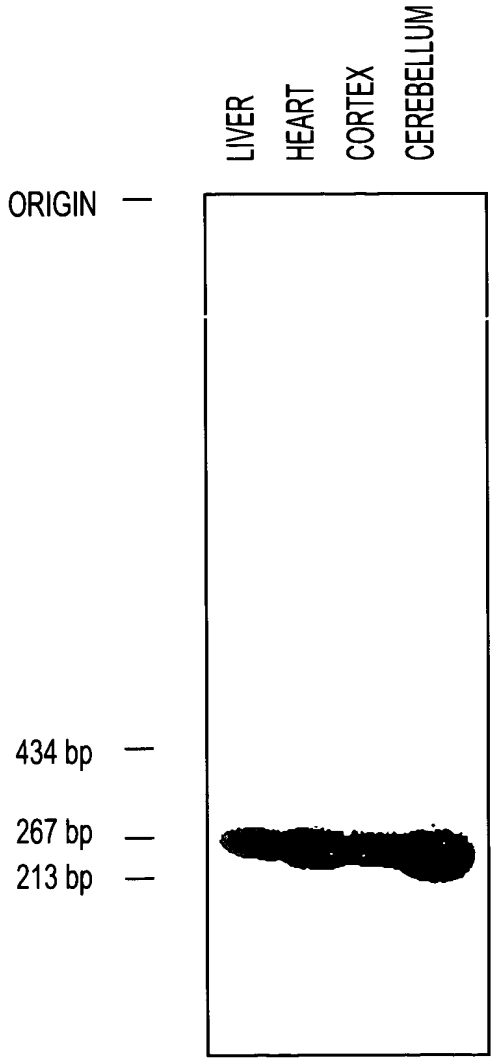


FIG. 11

```
                                                  10        20        30
EX                                          CACAAACTCAGAAACAGACACCATGGTGCACCTGA
                                            :::::::::::::::::::::::::::::::::::
RNBGLO  TGCTTCTGACATAGTTGTGTTGACTCACAAACTCAGAAACAGACACCATGGTGCACCTGA
                  10        20        30        40        50        60
                    40        50        60        70        80        90
EX      CTGATGCTGAGAAGGCTGCTGTTAATGGCCTGTGGGGAAAGGTGAACCCTGATGATGTTG
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
RNBGLO  CTGATGCTGAGAAGGCTGCTGTTAATGGCCTGTGGGGAAAGGTGAACCCTGATGATGTTG
                  70        80        90        100       110       120
                   100       110       120       130       140       150
EX      GTGGCGAGGCCCTGGGCAGGCTGCTGGTTGTCTACCCTTGGACCCAGAGGTACTTTGATA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
RNBGLO  GTGGCGAGGCCCTGGGCAGGCTGCTGGTTGTCTACCCTTGGACCCAGAGGTACTTTGATA
                  130       140       150       160       170       180
                   160       170       180       190       200       210
EX      GCTTTGGGGACCTGTCCTCTGCCTCTGCTATCATGGGTAACCCTAAGGTGAAGGCCCATG
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
RNBGLO  GCTTTGGGGACCTGTCCTCTGCCTCTGCTATCATGGGTAACCCTAAGGTGAAGGCCCATG
                  190       200       210       220       230       240
                   220       230       240       250       260       270
EX      GCAAGAAGGTGATAAACGCCTTCAATGATGGCCTGAAACACTTGGACAACCTCAAGGGCA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
RNBGLO  GCAAGAAGGTGATAAACGCCTTCAATGATGGCCTGAAACACTTGGACAACCTCAAGGGCA
                  250       260       270       280       290       300
                   280       290       300       310       320       330
EX      CCTTTGCTCATCTGAGTGAACTCCACTGTGACAAGCTGCATGTGGATCCTGAGAACTTCA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
RNBGLO  CCTTTGCTCATCTGAGTGAACTCCACTGTGACAAGCTGCATGTGGATCCTGAGAACTTCA
                  310       320       330       340       350       360
                   340       350       360       370       380       390
EX      GGCTCCTGGGCAATATGATTGTGATTGTGTTGGGCCACCACCTGGGCAAGGAATTCACCC
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
RNBGLO  GGCTCCTGGGCAATATGATTGTGATTGTGTTGGGCCACCACCTGGGCAAGGAATTCACCC
                  370       380       390       400       410       420
                   400       410       420       430       440       450
EX      CCTGTGCACAGGCTGCCTTCCAGAAGGTGGTGGCTGGAGTGGCCAGTGCCCTGGCTCACA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
RNBGLO  CCTGTGCACAGGCTGCCTTCCAGAAGGTGGTGGCTGGAGTGGCCAGTGCCCTGGCTCACA
                  430       440       450       460       470       480
                   460       470       480       490       500       510
EX      AGTACCACTAAACCTCTTTTCCTGCTCTTGTCTTTGTGCAATGGTCAATTGTTCCCAAGA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
RNBGLO  AGTACCACTAAACCTCTTTTCCTGCTCTTGTCTTTGTGCAATGGTCAATTGTTCCCAAGA
                  490       500       510       520       530       540
                   520       530       540       550       560       570
EX      GAGCATCTGTCAGTTGTTGTCAAAATGACAAAGACCTTTGAAAATCTGTCCTACTAATAA
        ::::::::::::::::::::::::::::::::::::::::::::::::::::::::::::
RNBGLO  GAGCATCTGTCAGTTGTTGTCAAAATGACAAAGACCTTTGAAAATCTGTCCTACTAATAA
                   580       590       600       610
EX      AAGGCATTTACTTTCACTGCAAAAAAAAAAAAAAAAAA
        ::::::::::::::::::
RNBGLO  AAGGCATTTACTTTCACTGC
```

FIG. 12

```
                                        10         20         30
EX                                      CACAAACTCAGAAACAGACACCATGGTGCACCTGA
                                                              M  V  H  L

      40         50         60         70         80         90
EX CTGATGCTGAGAAGGCTGCTGTTAATGGCCTGTGGGGAAAGGTGAACCCTGATGATGTTG
   T  D  A  E  K  A  A  V  N  G  L  W  G  K  V  N  P  D  D  V

     100        110        120        130        140        150
EX GTGGCGAGGCCCTGGGCAGGCTGCTGGTTGTCTACCCTTGGACCCAGAGGTACTTTGATA
   G  G  E  A  L  G  R  L  L  V  V  Y  P  W  T  Q  R  Y  F  D
     160        170        180        190        200        210
EX GCTTTGGGGACCTGTCCTCTGCCTCTGCTATCATGGGTAACCCTAAGGTGAAGGCCCATG
   S  F  G  D  L  S  S  A  S  A  I  M  G  N  P  K  V  K  A  H
     220        230        240        250        260        270
EX GCAAGAAGGTGATAAACGCCTTCAATGATGGCCTGAAACACTTGGACAACCTCAAGGGCA
   G  K  K  V  I  N  A  F  N  D  G  L  K  H  L  D  N  L  K  G
     280        290        300        310        320        330
EX CCTTTGCTCATCTGAGTGAACTCCACTGTGACAAGCTGCATGTGGATCCTGAGAACTTCA
   T  F  A  H  L  S  E  L  H  C  D  K  L  H  V  D  P  E  N  F
     340        350        360        370        380        390
EX GGCTCCTGGGCAATATGATTGTGATTGTGTTGGGCCACCACCTGGGCAAGGAATTCACCC
   R  L  L  G  N  M  I  V  I  V  L  G  H  H  L  G  K  E  F  T
     400        410        420        430        440        450
EX CCTGTGCACAGGCTGCCTTCCAGAAGGTGGTGGCTGGAGTGGCCAGTGCCCTGGCTCACA
   P  C  A  Q  A  A  F  Q  K  V  V  A  G  V  A  S  A  L  A  H
     460        470        480        490        500        510
EX AGTACCACTAAACCTCTTTTCCTGCTCTTGTCTTTGTGCAATGGTCAATTGTTCCCAAGA
   K  Y  H  *
     520        530        540        550        560        570
EX GAGCATCTGTCAGTTGTTGTCAAAATGACAAAGACCTTTGAAAATCTGTCCTACTAATAA

      580        590        600        610
EX AAGGCATTTACTTTCACTGCAAAAAAAAAAAAAAAAA
```

FIG. 13

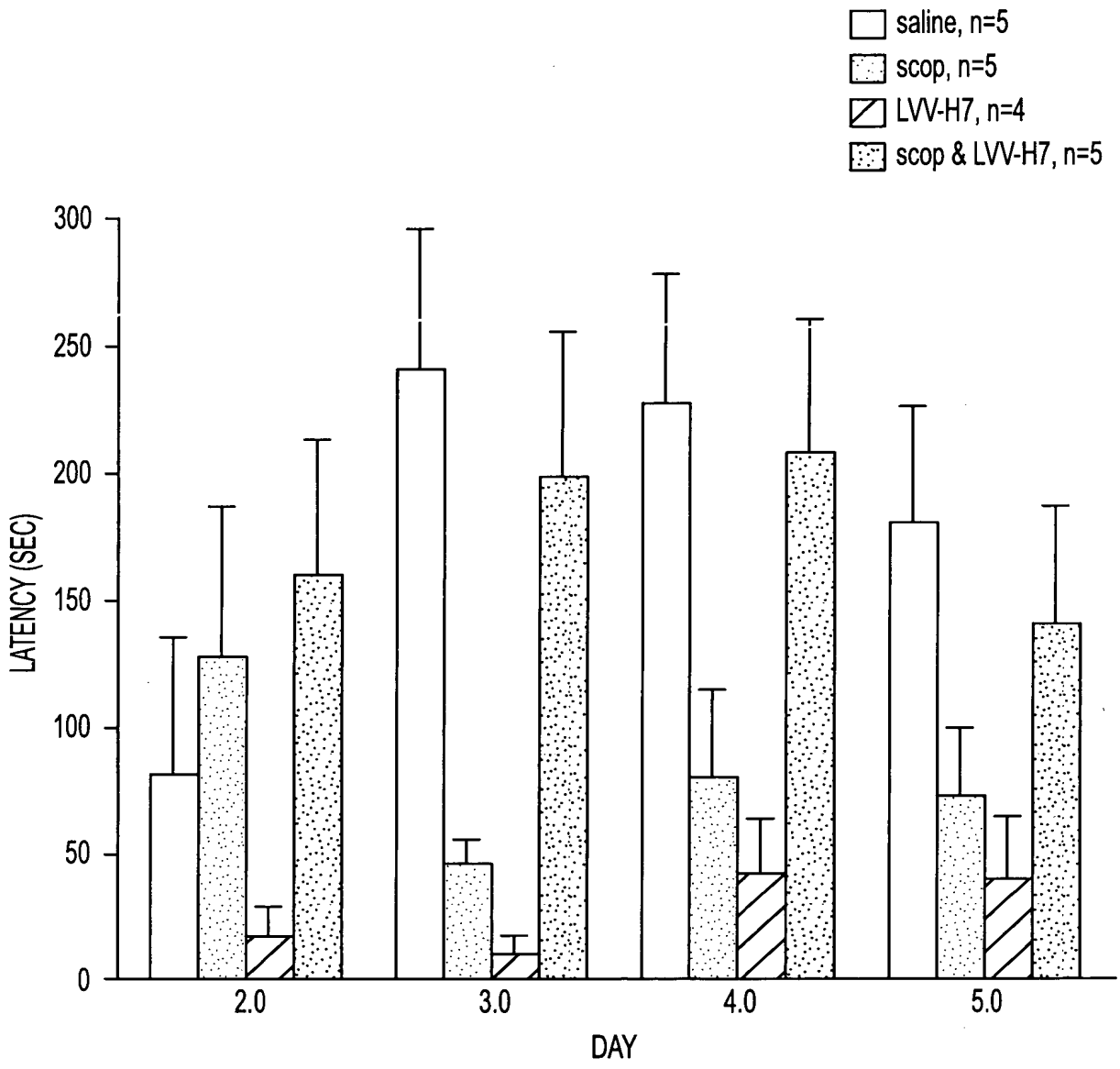
saline, n=5
scop, n=5
LVV-H7, n=4
scop & LVV-H7, n=5
LATENCY (SEC)
300
250
200
150
100
50
0
2.0
3.0
4.0
5.0
DAY

FIG. 14

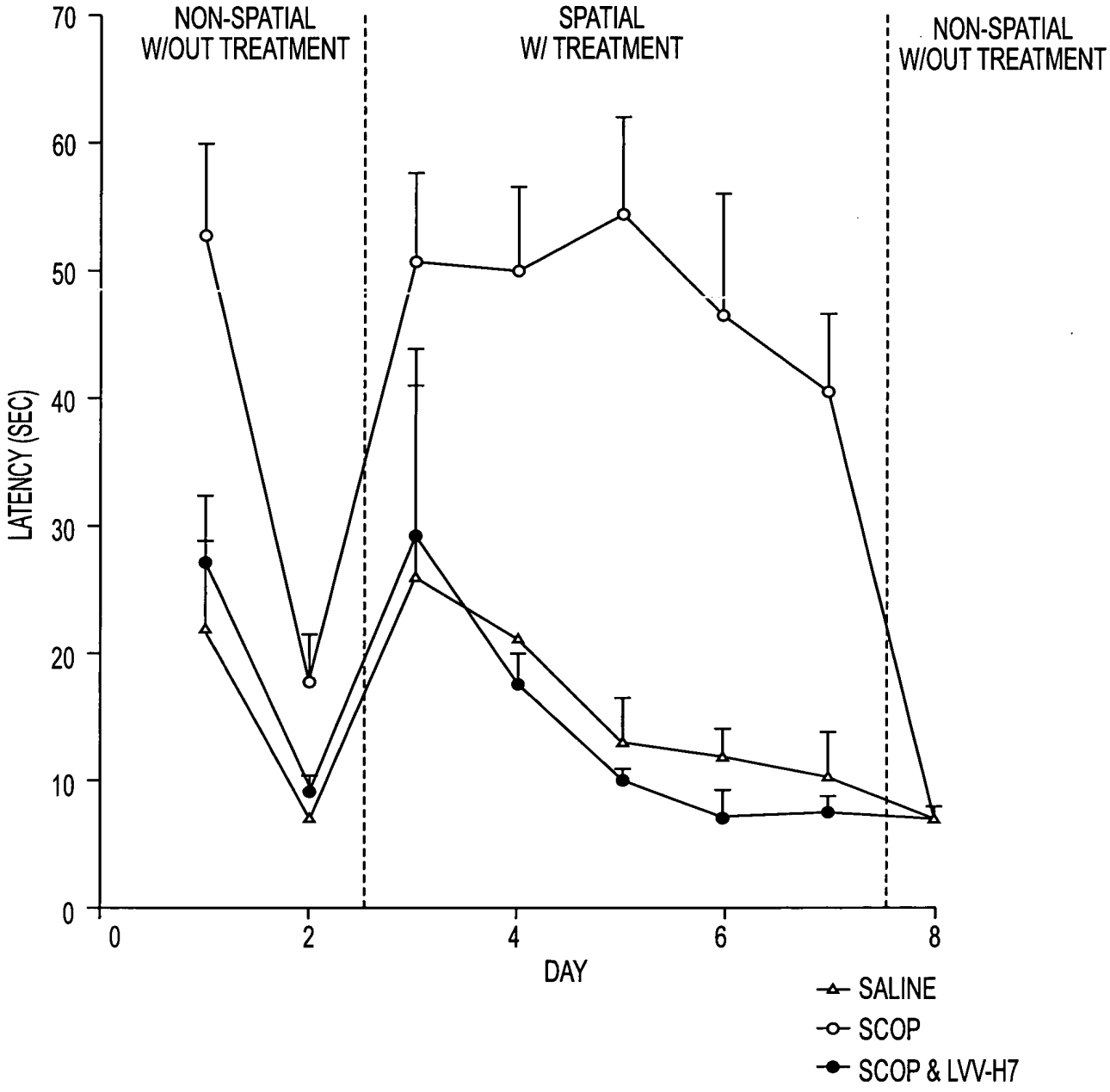
NON-SPATIAL
W/OUT TREATMENT
SPATIAL
W/ TREATMENT
NON-SPATIAL
W/OUT TREATMENT
LATENCY (SEC)
70
60
50
40
30
20
10
0
0
2
4
6
8
DAY
SALINE
SCOP
SCOP & LVV-H7

FIG. 15